

SEQUENCE LISTING

<110> AKZO Nobel N.V.

<120> novel *Brachyspira hyodysenteriae* vaccine

<130> Bhyovaccine

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 1614

<212> DNA

<213> *Brachyspira hyodysenteriae*

<220>

<221> CDS

<222> (1)..(1611)

<223>

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atg aaa aaa cta tat tca tta ttt ata ttt ata gct gta att tta ttt
Met Lys Lys Leu Tyr Ser Leu Phe Ile Phe Ile Ala Val Ile Leu Phe
1 5 10 15

48

att tat tca tgc gga agt tat ttt aat cct aaa tac tat ttt ttt aaa
Ile Tyr Ser Cys Gly Ser Tyr Phe Asn Pro Lys Tyr Phe Phe Lys
20 25 30

96

agt aaa gta gag aat aat gga agt tct gga agc tca ggc ggt aat tca
Ser Lys Val Glu Asn Asn Gly Ser Ser Gly Ser Gly Gly Asn Ser
35 40 45

144

gga ata tat ata cag cct ggt gaa gat gaa gat cct ttt aca gca cct Gly Ile Tyr Ile Gln Pro Gly Glu Asp Glu Asp Pro Phe Thr Ala Pro 50 55 60	192
aaa tat gca tct gag tgg tgg aat gat cct aat aat ggt gga ttt gat Lys Tyr Ala Ser Glu Trp Trp Asn Asp Pro Asn Asn Gly Gly Phe Asp 65 70 75 80	240
gct tcg gat ata gat aaa tgg ttt ttg aaa gtt gaa ttt tta gca aat Ala Ser Asp Ile Asp Lys Trp Phe Leu Lys Val Glu Phe Leu Ala Asn 85 90 95	288
gat tat cca agt tac aga ttt tta aca aaa agc gga aga aaa gca gga Asp Tyr Pro Ser Tyr Arg Phe Leu Thr Lys Ser Gly Arg Lys Ala Gly 100 105 110	336
cat gtt tgg gta gtt tct aat gaa caa tct cag gca tat tta gat caa His Val Trp Val Val Ser Asn Glu Gln Ser Gln Ala Tyr Leu Asp Gln 115 120 125	384
gga gaa gta tgc aat act aca gca gtt acc ggg gta tct ata aaa cca Gly Glu Val Cys Asn Thr Thr Ala Val Thr Gly Val Ser Ile Lys Pro 130 135 140	432
gta gca aat gta aca gga gta aca tat aca aaa tat aag gga ttg aat Val Ala Asn Val Thr Gly Val Thr Tyr Thr Lys Tyr Lys Gly Leu Asn 145 150 155 160	480
gca aga ttt ttc act cat gac gga gat tat cat aat gta tat cct gga Ala Arg Phe Phe Thr His Asp Gly Asp Tyr His Asn Val Tyr Pro Gly 165 170 175	528
aaa gat aag ata agc aga ttc tat ttt tat tat ttt aca ggt act ccg Lys Asp Lys Ile Ser Arg Phe Tyr Phe Tyr Tyr Phe Thr Gly Thr Pro 180 185 190	576
gaa atg gct aaa ttt tta gaa aat tgc tta ata gct gta gac aca tac Glu Met Ala Lys Phe Leu Glu Asn Cys Leu Ile Ala Val Asp Thr Tyr 195 200 205	624
tca aaa cta tta ttt tac tat gga aga cct caa agc gat tat cca aat Ser Lys Leu Leu Phe Tyr Tyr Gly Arg Pro Gln Ser Asp Tyr Pro Asn 210 215 220	672
cct cca agc tgg cag aag cct agt aat ttg gtt gat aaa tac tct cct Pro Pro Ser Trp Gln Lys Pro Ser Asn Leu Val Asp Lys Tyr Ser Pro 225 230 235 240	720
aca ggt tat tgg ata tct ata gat gaa ggt ata aat gat aag ggg cag Thr Gly Tyr Trp Ile Ser Ile Asp Glu Gly Ile Asn Asp Lys Gly Gln 245 250 255	768
aat tat cct ttt tat gaa tat gat cct gta gga tat gta aaa agc gat Asn Tyr Pro Phe Tyr Glu Tyr Asp Pro Val Gly Tyr Val Lys Ser Asp 260 265 270	816
ggt aca gtt gtt ata ttt gat tgg ttt gca aac aga tta aga gga aat	864

Gly Thr Val Val Ile Phe Asp Trp Phe Ala Asn Arg Leu Arg Gly Asn			
275	280	285	
cat aat aat gat cct ata aaa agt gat cct aaa gga gct att gtt cct			912
His Asn Asn Asp Pro Ile Lys Ser Asp Pro Lys Gly Ala Ile Val Pro			
290	295	300	
aat cct aat act aat cct tct gct tca act aca gga cgt tct cct tat			960
Asn Pro Asn Thr Asn Pro Ser Ala Ser Thr Thr Gly Arg Ser Pro Tyr			
305	310	315	320
gca ttc tat tcg cct tta gca caa aaa gat aaa act aaa ata act ata			1008
Ala Phe Tyr Ser Pro Leu Ala Gln Lys Asp Lys Thr Lys Ile Thr Ile			
325	330	335	
agt act aca aaa tta ata aat tat aca gtt ttc agt tat aaa tac agt			1056
Ser Thr Thr Lys Leu Ile Asn Tyr Thr Val Phe Ser Tyr Lys Tyr Ser			
340	345	350	
ata caa ata ttt ccg cct agt atg aaa gaa gaa aaa ctt cct tat gct			1104
Ile Gln Ile Phe Pro Pro Ser Met Lys Glu Glu Lys Leu Pro Tyr Ala			
355	360	365	
tat att gca tat gct tcc tat ggt gca gct tat caa aat gaa agc agc			1152
Tyr Ile Ala Tyr Ala Ser Tyr Gly Ala Ala Tyr Gln Asn Glu Ser Ser			
370	375	380	
aaa tct gta gag atg ata tct gat ata aat aaa gga gag cat tac gga			1200
Lys Ser Val Glu Met Ile Ser Asp Ile Asn Lys Gly Glu His Tyr Gly			
385	390	395	400
agt att aca aga ata agc act gta cct aaa ata gat aaa gac gga gga			1248
Ser Ile Thr Arg Ile Ser Thr Val Pro Lys Ile Asp Lys Asp Gly Gly			
405	410	415	
gag ttg gta aaa gaa gga tct aag tct ttt gaa tta tat ggt att gat			1296
Glu Leu Val Lys Glu Gly Ser Lys Ser Phe Glu Leu Tyr Gly Ile Asp			
420	425	430	
act aaa gat aca ttt ata gaa tta agt tta aaa cta att aaa aat gat			1344
Thr Lys Asp Thr Phe Ile Glu Leu Ser Leu Lys Leu Ile Lys Asn Asp			
435	440	445	
gaa aat aca gaa ttt gtt gat caa gga aca gca ggt act ggt cct tta			1392
Glu Asn Thr Glu Phe Val Asp Gln Gly Thr Ala Gly Thr Gly Pro Leu			
450	455	460	
gta tac ttt gat aaa aca gat cct ata ctt gta tta aaa tat gat aaa			1440
Val Tyr Phe Asp Lys Thr Asp Pro Ile Leu Val Leu Lys Tyr Asp Lys			
465	470	475	480
tct tct gac agc ttc aaa tac agc agt gta aaa gga aac aag caa ata			1488
Ser Ser Asp Ser Phe Lys Tyr Ser Ser Val Lys Gly Asn Lys Gln Ile			
485	490	495	
gaa gtt gac agc aat tta tca att aaa aga gga gag aat aaa gag ttt			1536
Glu Val Asp Ser Asn Leu Ser Ile Lys Arg Gly Glu Asn Lys Glu Phe			

500

505

510

aca gtt aaa ttt aaa gat cca aat aat gga aat gag ttt ggg gtt gta 1584
 Thr Val Lys Phe Lys Asp Pro Asn Asn Gly Asn Glu Phe Gly Val Val
 515 520 525

ttt aaa ata gat ttt gaa aaa ata tca tga 1614
 Phe Lys Ile Asp Phe Glu Lys Ile Ser
 530 535

<210> 2

<211> 537

<212> PRT

<213> Brachyspira hyodysenteriae

<400> 2

Met Lys Lys Leu Tyr Ser Leu Phe Ile Phe Ile Ala Val Ile Leu Phe
 1 5 10 15

Ile Tyr Ser Cys Gly Ser Tyr Phe Asn Pro Lys Tyr Tyr Phe Phe Lys
 20 25 30

Ser Lys Val Glu Asn Asn Gly Ser Ser Gly Ser Ser Gly Gly Asn Ser
 35 40 45

Gly Ile Tyr Ile Gln Pro Gly Glu Asp Glu Asp Pro Phe Thr Ala Pro
 50 55 60

Lys Tyr Ala Ser Glu Trp Trp Asn Asp Pro Asn Asn Gly Gly Phe Asp
 65 70 75 80

Ala Ser Asp Ile Asp Lys Trp Phe Leu Lys Val Glu Phe Leu Ala Asn
 85 90 95

Asp Tyr Pro Ser Tyr Arg Phe Leu Thr Lys Ser Gly Arg Lys Ala Gly
 100 105 110

His Val Trp Val Val Ser Asn Glu Gln Ser Gln Ala Tyr Leu Asp Gln
 115 120 125

Gly Glu Val Cys Asn Thr Thr Ala Val Thr Gly Val Ser Ile Lys Pro
 130 135 140

Val Ala Asn Val Thr Gly Val Thr Tyr Thr Lys Tyr Lys Gly Leu Asn
145 150 155 160

Ala Arg Phe Phe Thr His Asp Gly Asp Tyr His Asn Val Tyr Pro Gly
165 170 175

Lys Asp Lys Ile Ser Arg Phe Tyr Phe Tyr Tyr Phe Thr Gly Thr Pro
180 185 190

Glu Met Ala Lys Phe Leu Glu Asn Cys Leu Ile Ala Val Asp Thr Tyr
195 200 205

Ser Lys Leu Leu Phe Tyr Tyr Gly Arg Pro Gln Ser Asp Tyr Pro Asn
210 215 220

Pro Pro Ser Trp Gln Lys Pro Ser Asn Leu Val Asp Lys Tyr Ser Pro
225 230 235 240

Thr Gly Tyr Trp Ile Ser Ile Asp Glu Gly Ile Asn Asp Lys Gly Gln
245 250 255

Asn Tyr Pro Phe Tyr Glu Tyr Asp Pro Val Gly Tyr Val Lys Ser Asp
260 265 270

Gly Thr Val Val Ile Phe Asp Trp Phe Ala Asn Arg Leu Arg Gly Asn
275 280 285

His Asn Asn Asp Pro Ile Lys Ser Asp Pro Lys Gly Ala Ile Val Pro
290 295 300

Asn Pro Asn Thr Asn Pro Ser Ala Ser Thr Thr Gly Arg Ser Pro Tyr
305 310 315 320

Ala Phe Tyr Ser Pro Leu Ala Gln Lys Asp Lys Thr Lys Ile Thr Ile
325 330 335

Ser Thr Thr Lys Leu Ile Asn Tyr Thr Val Phe Ser Tyr Lys Tyr Ser
340 345 350

Ile Gln Ile Phe Pro Pro Ser Met Lys Glu Glu Lys Leu Pro Tyr Ala
355 360 365

Tyr Ile Ala Tyr Ala Ser Tyr Gly Ala Ala Tyr Gln Asn Glu Ser Ser
370 375 380

Lys Ser Val Glu Met Ile Ser Asp Ile Asn Lys Gly Glu His Tyr Gly
385 390 395 400

Ser Ile Thr Arg Ile Ser Thr Val Pro Lys Ile Asp Lys Asp Gly Gly
405 410 415

Glu Leu Val Lys Glu Gly Ser Lys Ser Phe Glu Leu Tyr Gly Ile Asp
420 425 430

Thr Lys Asp Thr Phe Ile Glu Leu Ser Leu Lys Leu Ile Lys Asn Asp
435 440 445

Glu Asn Thr Glu Phe Val Asp Gln Gly Thr Ala Gly Thr Gly Pro Leu
450 455 460

Val Tyr Phe Asp Lys Thr Asp Pro Ile Leu Val Leu Lys Tyr Asp Lys
465 470 475 480

Ser Ser Asp Ser Phe Lys Tyr Ser Ser Val Lys Gly Asn Lys Gln Ile
485 490 495

Glu Val Asp Ser Asn Leu Ser Ile Lys Arg Gly Glu Asn Lys Glu Phe
500 505 510

Thr Val Lys Phe Lys Asp Pro Asn Asn Gly Asn Glu Phe Gly Val Val
515 520 525

Phe Lys Ile Asp Phe Glu Lys Ile Ser
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<210> 3

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<212> DNA

<213> Brachyspira hyodysenteriae

<220>

<221> CDS

<222> (1)..(537)

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1 5 10 15		
gga tgt gaa act atg cag cct aaa aat aat gat aca att gta aaa aat	96	
Gly Cys Glu Thr Met Gln Pro Lys Asn Asn Asp Thr Ile Val Lys Asn		
20 25 30		
gat aat tca tct aat gaa gat aaa aaa gaa gaa act ata act aga gaa	144	
Asp Asn Ser Ser Asn Glu Asp Lys Lys Glu Thr Ile Thr Arg Glu		
35 40 45		
gat aca cca aaa atg aaa gtt aca gtt tat gga gca gat aaa gaa att	192	
Asp Thr Pro Lys Met Lys Val Thr Val Tyr Gly Ala Asp Lys Glu Ile		
50 55 60		
caa gct gtg gaa ata aat gat aaa act tat tat gta ata ggc gga aaa	240	
Gln Ala Val Glu Ile Asn Asp Lys Thr Tyr Val Ile Gly Gly Lys		
65 70 75 80		
gat gtt gag aat atg aca gaa gct gat ata aaa aaa tca tct tta gta	288	
Asp Val Glu Asn Met Thr Glu Ala Asp Ile Lys Lys Ser Ser Leu Val		
85 90 95		
gca cct tta aaa gtt aca gaa gaa act gtt aat ggt aca aga ggt ata	336	
Ala Pro Leu Lys Val Thr Glu Glu Thr Val Asn Gly Thr Arg Gly Ile		
100 105 110		
gtt gtt aca tat tat gat gta aaa gta ttc ttg ggt aaa aga aca gga	384	
Val Val Thr Tyr Tyr Asp Val Lys Val Phe Leu Gly Lys Arg Thr Gly		
115 120 125		
aca gga act atc gta gga ata ttc gag cct cag aaa aat gat tgg act	432	
Thr Gly Thr Ile Val Gly Ile Phe Glu Pro Gln Lys Asn Asp Trp Thr		
130 135 140		
aca gga aat gat ttg gat aga agt tta tct att caa ata aaa tta tct	480	
Thr Gly Asn Asp Leu Asp Arg Ser Leu Ser Ile Gln Ile Lys Leu Ser		
145 150 155 160		
aga aat ata gca ggt cct ata gat ata aaa aga gga agc ata tct tta	528	
Arg Asn Ile Ala Gly Pro Ile Asp Ile Lys Arg Gly Ser Ile Ser Leu		
165 170 175		
gca ttt aat taa	540	
Ala Phe Asn		

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<211> 179

<212> PRT

<213> Brachyspira hyodysenteriae

<400> 4

Met Phe Lys Lys Leu Phe Ile Val Val Gly Leu Met Ser Val Leu Ala
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Gly Cys Glu Thr Met Gln Pro Lys Asn Asn Asp Thr Ile Val Lys Asn
20 25 30

Asp Asn Ser Ser Asn Glu Asp Lys Lys Glu Glu Thr Ile Thr Arg Glu
35 40 45

Asp Thr Pro Lys Met Lys Val Thr Val Tyr Gly Ala Asp Lys Glu Ile
50 55 60

Gln Ala Val Glu Ile Asn Asp Lys Thr Tyr Tyr Val Ile Gly Gly Lys
65 70 75 80

Asp Val Glu Asn Met Thr Glu Ala Asp Ile Lys Lys Ser Ser Leu Val
85 90 95

Ala Pro Leu Lys Val Thr Glu Glu Thr Val Asn Gly Thr Arg Gly Ile
100 105 110

Val Val Thr Tyr Tyr Asp Val Lys Val Phe Leu Gly Lys Arg Thr Gly
115 120 125

Thr Gly Thr Ile Val Gly Ile Phe Glu Pro Gln Lys Asn Asp Trp Thr
130 135 140

Thr Gly Asn Asp Leu Asp Arg Ser Leu Ser Ile Gln Ile Lys Leu Ser
145 150 155 160

Arg Asn Ile Ala Gly Pro Ile Asp Ile Lys Arg Gly Ser Ile Ser Leu
165 170 175

Ala Phe Asn